

WEST Search History

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DATE: Tuesday, September 20, 2005

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[Hit Count](#)

DB=PGPB,USPT,EPAB; PLUR=YES; OP=ADJ

<input type="checkbox"/>	L13	L3 and L9	0
<input type="checkbox"/>	L12	L9 and L11	0
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<input type="checkbox"/>	L10	L9 and L7	29
<input type="checkbox"/>	L9	(536/23.1)![CCLS]	12263
<input type="checkbox"/>	L8	L7 and L1	1
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<input type="checkbox"/>	L3	L2.ab.	52
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<input type="checkbox"/>	L1	dai.in.	2900

END OF SEARCH HISTORY

us-10-653-681b-1.oligo.rng

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 9, 2005, 12:07:39 ; Search time 698 Seconds
(without alignments)
9244.295 Million cell updates/sec

Title: US-10-653-681B-1

Perfect score: 1090

Sequence: 1 caaaaacagcaacagaaaagc.....ataaaaaaaaataataatcat 1090

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 4390206 seqs, 2959870667 residues

Word size : 0

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : N_Geneseq_16Dec04:*

1: geneseqn1980s:*

2: geneseqn1990s:*

3: geneseqn2000s:*

4: geneseqn2001as:*

5: geneseqn2001bs:*

6: geneseqn2002as:*

7: geneseqn2002bs:*

8: geneseqn2003as:*

9: geneseqn2003bs:*

10: geneseqn2003cs:*

11: geneseqn2003ds:*

12: geneseqn2004as:*

13: geneseqn2004bs:*

Pred. N. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	%	Description
1	780	71.6	1337	5	AAS68608		Aas68608 DNA encod
2	780	71.6	1337	10	ADD71032		Add71032 Human ald
3	773	70.9	1549	12	ADK70274		Adk70274 Respirato
4	729	66.9	1508	3	AAC98140		Aac98140 Human col
5	729	66.9	1560	12	ADJ75119		Adj75119 Marker ge
6	729	66.9	1560	12	ADN04246		Adn04246 Antipsori
7	729	66.9	1560	13	ACN38728		Acn38728 Tumour-as
8	729	66.9	1560	13	ADS85007		Ads85007 Human ato
9	664	60.9	1316	5	AAF68405		Aaf68405 Human lun
10	664	60.9	1316	6	ABK38316		Abk38316 cDNA enco

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11	664	60.9	1316	7	ADS73134	Ads73134 Human kid
12	664	60.9	1316	8	ACA10645	Aca10645 Human lun
13	664	60.9	1316	8	ABX99596	Abx99596 Lung canc
14	664	60.9	1316	10	ADH45842	Adh45842 Human lun
15	664	60.9	1316	12	ADE72379	Ade72379 Human lun
16	664	60.9	1316	13	ADJ19761	Adj19761 Human lun
17	529	48.5	770	13	ADR98739	Adr98739 Lung spec
18	529	48.5	1621	12	ADH13722	Adh13722 Human ENZ
c 19	389	35.7	558	10	ABZ84625	Abz84625 Toxicolog
20	328	30.1	364	4	AAS39335	Aas39335 Novel hum
21	316	29.0	585	2	AAZ24592	Aaz24592 Human lun
22	316	29.0	585	3	AAC65831	Aac65831 Human lun
23	316	29.0	585	6	ABL49050	Ab149050 Human lun
24	316	29.0	585	6	ABQ92236	Abq92236 Human lun
25	316	29.0	585	9	ADA28651	Ada28651 Human lun
26	316	29.0	585	10	ADE53611	Ade53611 Human lun
27	316	29.0	585	10	ADH36746	Adh36746 Human lun
28	316	29.0	585	12	ADM56549	Adm56549 Human lun
29	316	29.0	585	12	ADN89593	Adn89593 Human lun
c 30	316	29.0	857	9	ADA28650	Ada28650 Human lun
c 31	316	29.0	858	2	AAZ24591	Aaz24591 Human lun
c 32	316	29.0	858	3	AAC65830	Aac65830 Human lun
c 33	316	29.0	858	6	ABL49049	Ab149049 Human lun
c 34	316	29.0	858	6	ABQ92235	Abq92235 Human lun
c 35	316	29.0	858	10	ADE53610	Ade53610 Human lun
c 36	316	29.0	858	10	ADH36745	Adh36745 Human lun
c 37	316	29.0	858	12	ADM56548	Adm56548 Human lun
c 38	316	29.0	858	12	ADN89592	Adn89592 Human lun
39	304	27.9	356	4	AAS39333	Aas39333 Novel hum
40	252	23.1	1396	5	AAS91091	Aas91091 DNA encod
41	249	22.8	861	5	AAS68606	Aas68606 DNA encod
42	235	21.6	830	4	AAI92428	Aai92428 Human pol
43	183	16.8	540	12	ADP28822	Adp28822 Human sec
44	174	16.0	857	13	ADR98738	Adr98738 Lung spec
c 45	159	14.6	198	12	ACH84956	Ach84956 Human gen

RESULT 9

AAF68405

ID AAF68405 standard; cDNA; 1316 BP.

XX

AC AAF68405;

XX

DT 12-APR-2001 (first entry)

XX

DE Human lung tumour protein related nucleotide sequence SEQ ID NO:323.

XX

KW Human; lung cancer; lung tumour; lung tumour protein; gene therapy;
KW lung cancer antigen; lung tumour-specific antigen; diagnosis; vaccine;
KW cytostatic; antisense inhibition; ss.

XX

OS Homo sapiens.

XX

PN WO200100828-A2.

XX

PD 04-JAN-2001.

XX

PF 30-JUN-2000; 2000WO-US018061.

XX

PR 30-JUN-1999; 99US-00346492.

PR 15-OCT-1999; 99US-00419356.

PR 17-DEC-1999; 99US-00466867.

PR 30-DEC-1999; 99US-00476300.

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PR 06-MAR-2000; 2000US-00519642.
PR 22-MAR-2000; 2000US-00533077.
PR 10-APR-2000; 2000US-00546259.
PR 27-APR-2000; 2000US-00560406.
PR 05-JUN-2000; 2000US-00589184.

XX
PA (CORI-) CORIXA CORP.

XX
PI Wang T, Bangur CS, Lodes MJ, Fanger GR, Vedvick TS, Carter D;
PI Retter MW, Mannion J;

XX
DR WPI; 2001-071488/08.

XX
PT Lung tumor-associated proteins and the nucleic acids that encode them,
PT useful for preventing, diagnosing and treating lung cancer.

XX
PS Example 1; Page 249-250; 436pp; English.

XX
The present invention describes immunogenic portions of lung tumour-
CC associated proteins (I) and the nucleic acids (NAs) that encode them. (I)
CC have cytostatic activity and can be used in gene therapy, antisense
CC inhibition and in vaccines. The NAs and the lung tumour-associated
CC proteins they encode may be used in the prevention, treatment and
CC diagnosis of diseases associated with their inappropriate expression,
CC especially lung cancers. For example, the NAs may be administered to
CC treat diseases by rectifying mutations or deletions in a patient's genome
CC that affect the activity of the protein by expressing inactive proteins
CC or to supplement the patients own production of (I). Additionally, the
CC NAs may be used to produce the lung-tumour associated protein, according
CC to standard recombinant DNA methodology. Conversely, antisense NA
CC molecules may be administered to down regulate protein expression by
CC binding with the cells own genes and preventing their expression. The NA
CC and complementary sequences may also be used as DNA probes in diagnostic
CC assays to detect and quantitate the presence of similar NA sequences in
CC samples, and hence which patients may be in need of treatment for lung
CC cancer. The (I) may be used as antigens in the production of antibodies
CC and in assays to identify modulators (agonists and antagonists) of the
CC expression and activity of the protein. AAF68083 to AAF68878 and AAB76848
CC to AAB76878 represent human lung tumour protein related nucleotide and
CC protein sequences which are used in the exemplification of the present
CC invention

XX
SQ Sequence 1316 BP; 385 A; 299 C; 308 G; 324 T; 0 U; 0 Other;

Query Match 60.9%; Score 664; DB 5; Length 1316;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 764; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy	311	CCACTTCCAGATCGAGAAGCTTGAACAAACCTGGACTGAAATATAAACCAAGTGACTAA	370
Db	528	CCACTTCCAGATCGAGAAGCTTGAACAAACCTGGACTGAAATATAAACCAAGTGACTAA	587
Qy	371	CCAGGTTGAGTGTACCCATACCTCACGCAGGAGAAACTGATCCAGTACTGCCACTCAA	430
Db	588	CCAGGTTGAGTGTACCCATACCTCACACAGGAGAAACTGATCCAGTACTGCCACTCAA	647
Qy	431	GGGCATCACCGTTACGGCTACAGCCCCCTGGCTCTCCGGATAGACCTTGGCCAAGCC	490
Db	648	GGGCATCACCGTTACGGCTACAGCCCCCTGGCTCTCCGGATAGACCTTGGCCAAGCC	707
Qy	491	AGAAGACCCCTCCCTGCTGGAGGATCCAAGATTAAGGAGATTGCTGCAAAGCACAAAAA	550
Db	708	AGAAGACCCCTCCCTGCTGGAGGATCCAAGATTAAGGAGATTGCTGCAAAGCACAAAAA	767

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Qy	551	AACCGCAGCCCAGGTTCTGATCCGTTCCATATCCAGAGGAATGTGATTGTCATCCCCAA	610
Db	768	AACCGCAGCCCAGGTTCTGATCCGTTCCATATCCAGAGGAATGTGATTGTCATCCCCAA	827
Qy	611	GTCTGTGACACCAGCACGCATTGTTGAGAACATTCAAGGCTTTGACTTTAAATTGAGTGA	670
Db	828	GTCTGTGACACCAGCACGCATTGTTGAGAACATTCAAGGCTTTGACTTTAAATTGAGTGA	887
Qy	671	TGAGGAGATGGCAACCATACTCAGCTTCAACAGAAAATGGAGGGCCTGTAACGTGTTGCA	730
Db	888	TGAGGAGATGGCAACCATACTCAGCTTCAACAGAAAATGGAGGGCCTGTAACGTGTTGCA	947
Qy	731	ATCCTCTCATTTGGAAGACTATCCCTTCGATGCAGAACATTGAGGTTGAATCTCCTGGTG	790
Db	948	ATCCTCTCATTTGGAAGACTATCCCTTCATGCAGAACATTGAGGTTGAATCTCCTGGTG	1007
Qy	791	AGATTATAACAGGAGATTCTCTTCTCGCTGAAGTGTGACTACCTCCACTCATGTCCCAT	850
Db	1008	AGATTATAACAGGAGATTCTCTTCTCGCTGAAGTGTGACTACCTCCACTCATGTCCCAT	1067
Qy	851	TTTAGCCAAGCTTATTAAGATCACAGTGAACCTAGTCCTGTTATAGACGAGAACATCGAGG	910
Db	1068	TTTAGCCAAGCTTATTAAGATCACAGTGAACCTAGTCCTGTTATAGACGAGAACATCGAGG	1127
Qy	911	TGCTGTTTAGACATTTATTCTGTATGTTCAACTAGGATCAGAACATACAGAAAAGCA	970
Db	1128	TGCTGTTTAGACATTTATTCTGTATGTTCAACTAGGATCAGAACATACAGAAAAGCA	1187
Qy	971	TGGCTTGAATAAGGAAATGACAATTTCACCTTATCTGATCAGAACAAATGTTATT	1030
Db	1188	TGGCTTGAATAAGGAAATGACAATTTCACCTTATCTGATCAGAACAAATGTTATT	1247
Qy	1031	AGCATCAGAAACTCTGCCAACACTGAGGATGTAAGATCAATAAAA	1076
Db	1248	AGCATCAGAAACTCTGCCAACACTGAGGATGTAAGATCAATAAAA	1293

RESULT 10

ABK38316

ID ABK38316 standard; cDNA; 1316 BP.

XX

AC ABK38316;

XX

DT 21-MAY-2002 (first entry)

XX

DE cDNA encoding clone #18973 (L516S) of lung tumour protein.

XX

KW Lung tumour; cancer; T cell; immune response stimulator; cytostatic; gene; ss.

XX

OS Homo sapiens.

XX

PN WO200204514-A2.

XX

PD 17-JAN-2002.

XX

PF 10-JUL-2001; 2001WO-US022058.

XX

PR 11-JUL-2000; 2000US-00614124.

PR 29-AUG-2000; 2000US-00651563.

PR 08-SEP-2000; 2000US-00658824.

PR 26-SEP-2000; 2000US-00671325.

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PR 06-OCT-2000; 2000US-00677419.
PR 30-OCT-2000; 2000US-00702705.
PR 13-DEC-2000; 2000US-00736457.
PR 03-MAY-2001; 2001US-00849626.

XX
PA (CORI-) CORIXA CORP.
XX

PI Wang T, Watanabe Y, Henderson RA, Johnson JC, Retter MW;
PI Marnerakis M, Carter D, Fanger GR, Vedvick TS, Bangur CS, Mcnabb A;
PI Wang A, Fanger N, Switzer A, Mcneill PD, Clapper JD;

XX
DR WPI; 2002-164634/21.

XX
PT Novel polynucleotide encoding a lung tumor polypeptide useful for
PT stimulating and/or expanding T cells specific for a tumor protein.

XX
PS Example 1; SEQ ID NO 323; 223pp; English.

XX
CC The invention describes an isolated polynucleotide and polypeptide useful
CC for stimulating and/or expanding T cells specific for a tumour protein
CC for determining the presence of a cancer in a patient. A composition
CC containing the polynucleotide and/or polypeptide is useful for treating a
CC lung cancer in a patient. The polypeptide is useful for removing tumour
CC cells from a biological sample. The polynucleotide is also useful as
CC probe or primer to detect the level of mRNA encoding a tumour protein.
CC This sequence encodes a lung tumour associated protein or protein
CC fragment, described in the method of the invention. Note: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format directly from WIPO at
CC ftp://wipo.int/pub/published_pct_sequences

XX
SQ Sequence 1316 BP; 385 A; 299 C; 308 G; 324 T; 0 U; 0 Other;

Query Match 60.9%; Score 664; DB 6; Length 1316;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 764; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy	311	CCACTTCCAGATCGAGAACGCTTGAACAAACCTGGACTGAAATATAAACCAAGTGACTAA	370
Db	528	CCACTTCCAGATCGAGAACGCTTGAACAAACCTGGACTGAAATATAAACCAAGTGACTAA	587
Qy	371	CCAGGTTGAGTGTACCCATACCTCACGCAGGAGAAACTGATCCAGTACTGCCACTCAA	430
Db	588	CCAGGTTGAGTGTACCCATACCTCACACAGGAGAAACTGATCCAGTACTGCCACTCAA	647
Qy	431	GGGCATCACCGTTACGGCCTACAGCCCCCTGGCTCTCGGATAGACCTTGGCCAAGCC	490
Db	648	GGGCATCACCGTTACGGCCTACAGCCCCCTGGCTCTCGGATAGACCTTGGCCAAGCC	707
Qy	491	AGAAGACCCCTCCCTGCTGGAGGATCCAAGATTAAGGAGATTGCTGCAAAGCACAAAAA	550
Db	708	AGAAGACCCCTCCCTGCTGGAGGATCCAAGATTAAGGAGATTGCTGCAAAGCACAAAAA	767
Qy	551	AACCGCAGCCCAGGTTCTGATCCGTTCCATATCCAGAGGAATGTGATTGTCATCCCCAA	610
Db	768	AACCGCAGCCCAGGTTCTGATCCGTTCCATATCCAGAGGAATGTGATTGTCATCCCCAA	827
Qy	611	GTCTGTGACACCAGCACGCATTGTTGAGAACATTCAAGGTCTTGACTTTAAATTGAGTGA	670
Db	828	GTCTGTGACACCAGCACGCATTGTTGAGAACATTCAAGGTCTTGACTTTAAATTGAGTGA	887
Qy	671	TGAGGAGATGGCAACCATACTCAGCTAACAGAAACTGGAGGGCTGTAACGTGTTGCA	730

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Db	888	TGAGGAGATGGCAACCATACTCAGCTCAACAGAACTGGAGGGCCTGTAACGTGTTGCA	947
Qy	731	ATCCTCTCATTTGGAAGACTATCCCTCGATGCAGAATTGAGGTTGAATCTCCTGGTG	790
Db	948	ATCCTCTCATTTGGAAGACTATCCCTCAATGCAGAATTGAGGTTGAATCTCCTGGTG	1007
Qy	791	AGATTATAACAGGAGATTCTCTTCTCGCTGAAGTGTGACTACCTCCACTCATGTCCCAT	850
Db	1008	AGATTATAACAGGAGATTCTCTTCTCGCTGAAGTGTGACTACCTCCACTCATGTCCCAT	1067
Qy	851	TTTAGCCAAGCTTATTAAGATCACAGTGAACCTAGTCCTGTTAGACGAGAACATCGAGG	910
Db	1068	TTTAGCCAAGCTTATTAAGATCACAGTGAACCTAGTCCTGTTAGACGAGAACATCGAGG	1127
Qy	911	TGCTGTTTAGACATTTATTCGTATGTTCAACTAGGATCAGAATATCACAGAAAAGCA	970
Db	1128	TGCTGTTTAGACATTTATTCGTATGTTCAACTAGGATCAGAATATCACAGAAAAGCA	1187
Qy	971	TGGCTTGAATAAGGAAATGACAATTTTCCACTTATCTGATCAGAACAAATGTTATTA	1030
Db	1188	TGGCTTGAATAAGGAAATGACAATTTTCCACTTATCTGATCAGAACAAATGTTATTA	1247
Qy	1031	AGCATCAGAAACTCTGCCAACACTGAGGATGAAAGATCAATAAAA	1076
Db	1248	AGCATCAGAAACTCTGCCAACACTGAGGATGAAAGATCAATAAAA	1293

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OM nucleic - nucleic search, using sw model

Run on: August 9, 2005, 11:49:49 ; Search time 5147 Seconds
(without alignments)
10261.548 Million cell updates/sec

Title: US-10-653-681B-1
Perfect score: 1090

Sequence: 1 caaaaacagcaacagaaagc.....ataaaaaaaaaataataatcat 1090

Scoring table: OLIGO_NUC
Gapext 60.0 , Gapext 60.0

Searched: 4708233 seqs, 24227607955 residues

Word size : 0

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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2: gb_htg:
3: gb_in:
4: gb_om:
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13: gb_un:
14: gb_vi:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Result No.	Score	Query Match	Length	DB	ID	Description
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3	729	66.9	1551	9	BC008837	BC008837 Homo sapi
4	729	66.9	1560	6	CQ776685	CQ776685 Sequence
5	721	66.1	1611	9	AF524864	AF524864 Homo sapi
6	664	60.9	1316	6	AR272611	AR272611 Sequence
7	664	60.9	1316	6	AR276192	AR276192 Sequence
8	664	60.9	1316	6	AR406467	AR406467 Sequence
9	664	60.9	1316	6	AR440317	AR440317 Sequence
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11	664	60.9	1316	6	AR543128	AR543128 Sequence
12	664	60.9	1316	6	AX062696	AX062696 Sequence
13	664	60.9	1316	6	AX367613	AX367613 Sequence
14	664	60.9	1316	9	AF052577	AF052577 Homo sapi
15	574	52.7	574	9	AF044961	AF044961 Homo sapi
16	410	37.6	951	9	BT006794	BT006794 Homo sapi
17	410	37.6	951	12	BT007750	BT007750 Synthetic
18	409	37.5	948	9	CR541801	CR541801 Homo sapi
19	331	30.4	163631	9	AC009276	AC009276 Homo sapi
c 20	331	30.4	170919	9	AC078847	AC078847 Homo sapi
c 21	331	30.4	177373	2	AP002452	AP002452 Homo sapi
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23	328	30.1	364	6	AX247463	AX247463 Sequence
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31	316	29.0	585	6	AR476374	AR476374 Sequence
32	316	29.0	585	6	AR486565	AR486565 Sequence
33	316	29.0	585	6	AR541068	AR541068 Sequence
34	316	29.0	585	6	AX365699	AX365699 Sequence
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c 38	316	29.0	858	6	AR220482	AR220482 Sequence
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ALIGNMENTS

RESULT 1
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 LOCUS CQ718316 1336 bp DNA linear PAT 03-FEB-
 2004
 DEFINITION Sequence 4250 from Patent WO02068579.
 ACCESSION CQ718316
 VERSION CQ718316.1 GI:42279173
 KEYWORDS

SOURCE *Homo sapiens* (human)

ORGANISM *Homo sapiens*
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; *Homo*.

REFERENCE 1

AUTHORS Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W.

TITLE Kits, such as nucleic acid arrays, comprising a majority of
 humanexons or transcripts, for detecting expression and other uses
 thereof

JOURNAL Patent: WO 02068579-A 4250 06-SEP-2002;
 PE Corporation (NY) (US)

FEATURES Location/Qualifiers

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 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"

ORIGIN

Query Match 71.6%; Score 780; DB 6; Length 1336;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 780; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 311 CCACCTCCAGATCGAGAAGCTCTTGAACAAACCTGGACTGAAATATAAACCAAGTGACTAA 370
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Db 557 CCACCTCCAGATCGAGAAGCTCTTGAACAAACCTGGACTGAAATATAAACCAAGTGACTAA 616

Qy 371 CCAGGTTGAGTGTACCCATACCTCACGCAGGAGAAACTGATCCAGTACTGCCACTCCAA 430
 |||||||

Db 617 CCAGGTTGAGTGTACCCATACCTCACGCAGGAGAAACTGATCCAGTACTGCCACTCCAA 676

Qy 431 GGGCATCACCGTTACGGCCTACAGCCCCCTGGGCTCTCCGGATAGACCTTGGCCAAGCC 490
 |||||||

Db 677 GGGCATCACCGTTACGGCCTACAGCCCCCTGGGCTCTCCGGATAGACCTTGGCCAAGCC 736

Qy 491 AGAAGACCCTTCCCTGCTGGAGGATCCAAGATTAAGGAGATTGCTGCAAAGCACAAAAA 550
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Db 737 AGAAGACCCTTCCCTGCTGGAGGATCCAAGATTAAGGAGATTGCTGCAAAGCACAAAAA 796

Qy 551 AACCGCAGCCCAGGTTCTGATCCGTTCCATATCCAGAGGAATGTGATTGTCATCCCCAA 610
 |||||||

Db 797 AACCGCAGCCCAGGTTCTGATCCGTTCCATATCCAGAGGAATGTGATTGTCATCCCCAA 856

Qy 611 GTCTGTGACACCAAGCACGCATTGTTGAGAACATTCAAGGTCTTGACTTTAAATTGAGTGA 670
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Db 857 GTCTGTGACACCAAGCACGCATTGTTGAGAACATTCAAGGTCTTGACTTTAAATTGAGTGA 916

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Qy 851 TTTAGCCAAGCTTATTAAGATCACAGTGAACCTAGTCCTGTTATAGACGAGAATCGAGG 910
|||
Db 1097 TTTAGCCAAGCTTATTAAGATCACAGTGAACCTAGTCCTGTTATAGACGAGAATCGAGG
1156

Qy 911 TGCTGTTTAGACATTATTCCTGTATGTTCAACTAGGATCAGAATATCACAGAAAGCA 970
|||
Db 1157 TGCTGTTTAGACATTATTCCTGTATGTTCAACTAGGATCAGAATATCACAGAAAAGCA
1216

Qy 971 TGGCTTGAATAAGGAAATGACAATTTCCTACTTATCTGATCAGAACAAATGTTATTA
1030
|||
Db 1217 TGGCTTGAATAAGGAAATGACAATTTCCTACTTATCTGATCAGAACAAATGTTATTA
1276

Qy 1031 AGCATCAGAAACTCTGCCAACACTGAGGATGTAAAGATCAATAAAAAAAATAATAATCAT
1090
|||
Db 1277 AGCATCAGAAACTCTGCCAACACTGAGGATGTAAAGATCAATAAAAAAAATAATAATCAT
1336

us-10-653-681b-1.oligo.rng

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OM nucleic - nucleic search, using sw model

Run on: August 9, 2005, 12:07:39 ; Search time 698 Seconds
(without alignments)
9244.295 Million cell updates/sec

Title: US-10-653-681B-1

Perfect score: 1090

Sequence: 1 caaaaacagcaacagaaagc.....ataaaaaaaaataataatcat 1090

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 4390206 seqs, 2959870667 residues

word size : 0

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : N_Geneseq_16Dec04:*

1: geneseqn1980s:*

2: geneseqn1990s:*

3: geneseqn2000s:*

4: geneseqn2001as:*

5: geneseqn2001bs:*

6: geneseqn2002as:*

7: geneseqn2002bs:*

8: geneseqn2003as:*

9: geneseqn2003bs:*

10: geneseqn2003cs:*

11: geneseqn2003ds:*

12: geneseqn2004as:*

13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	%	Description
1	780	71.6	1337	5	AAS68608		Aas68608 DNA encod
2	780	71.6	1337	10	ADD71032		Add71032 Human ald
3	773	70.9	1549	12	ADK70274		Adk70274 Respirato
4	729	66.9	1508	3	AAC98140		Aac98140 Human col
5	729	66.9	1560	12	ADJ75119		Adj75119 Marker ge
6	729	66.9	1560	12	ADN04246		Adn04246 Antipsori
7	729	66.9	1560	13	ACN38728		Acn38728 Tumour-as
8	729	66.9	1560	13	ADS85007		Ads85007 Human ato
9	664	60.9	1316	5	AAF68405		Aaf68405 Human lun
10	664	60.9	1316	6	ABK38316		Abk38316 cDNA enco

us-10-653-681b-1.oligo.rng

11	664	60.9	1316	7	ADS73134	Ads73134 Human kid
12	664	60.9	1316	8	ACA10645	Aca10645 Human lun
13	664	60.9	1316	8	ABX99596	Abx99596 Lung canc
14	664	60.9	1316	10	ADH45842	Adh45842 Human lun
15	664	60.9	1316	12	ADE72379	Ade72379 Human lun
16	664	60.9	1316	13	ADJ19761	Adj19761 Human lun
17	529	48.5	770	13	ADR98739	Adr98739 Lung spec
18	529	48.5	1621	12	ADH13722	Adh13722 Human ENZ
c 19	389	35.7	558	10	ABZ84625	Abz84625 Toxicolog
20	328	30.1	364	4	AAS39335	Aas39335 Novel hum
21	316	29.0	585	2	AAZ24592	Aaz24592 Human lun
22	316	29.0	585	3	AAC65831	Aac65831 Human lun
23	316	29.0	585	6	ABL49050	Ab149050 Human lun
24	316	29.0	585	6	ABQ92236	Abq92236 Human lun
25	316	29.0	585	9	ADA28651	Ada28651 Human lun
26	316	29.0	585	10	ADE53611	Ade53611 Human lun
27	316	29.0	585	10	ADH36746	Adh36746 Human lun
28	316	29.0	585	12	ADM56549	Adm56549 Human lun
29	316	29.0	585	12	ADN89593	Adn89593 Human lun
c 30	316	29.0	857	9	ADA28650	Ada28650 Human lun
c 31	316	29.0	858	2	AAZ24591	Aaz24591 Human lun
c 32	316	29.0	858	3	AAC65830	Aac65830 Human lun
c 33	316	29.0	858	6	ABL49049	Ab149049 Human lun
c 34	316	29.0	858	6	ABQ92235	Abq92235 Human lun
c 35	316	29.0	858	10	ADE53610	Ade53610 Human lun
c 36	316	29.0	858	10	ADH36745	Adh36745 Human lun
c 37	316	29.0	858	12	ADM56548	Adm56548 Human lun
c 38	316	29.0	858	12	ADN89592	Adn89592 Human lun
39	304	27.9	356	4	AAS39333	Aas39333 Novel hum
40	252	23.1	1396	5	AAS91091	Aas91091 DNA encod
41	249	22.8	861	5	AAS68606	Aas68606 DNA encod
42	235	21.6	830	4	AAI92428	Aai92428 Human pol
43	183	16.8	540	12	ADP28822	Adp28822 Human sec
44	174	16.0	857	13	ADR98738	Adr98738 Lung spec
c 45	159	14.6	198	12	ACH84956	Ach84956 Human gen

ALIGNMENTS

RESULT 1

AAS68608

ID AAS68608 standard; cDNA; 1337 BP.

XX

AC AAS68608;

XX

DT 13-FEB-2002 (first entry)

XX

DE DNA encoding novel human diagnostic protein #4412.

XX

KW Human; chromosome mapping; gene mapping; gene therapy; forensic;

KW food supplement; medical imaging; diagnostic; genetic disorder; ss.

XX

OS Homo sapiens.

XX

PN WO200175067-A2.

XX

PD 11-OCT-2001.

XX

PF 30-MAR-2001; 2001WO-US008631.

XX

PR 31-MAR-2000; 2000US-00540217.

PR 23-AUG-2000; 2000US-00649167.

XX
PA (HYSEQ INC.
XX
PI Drmanac RT, Liu C, Tang YT;
XX
DR WPI; 2001-639362/73.
DR P-PSDB; ABG04421.
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity.
XX
PS Claim 1; SEQ ID NO 4412; 103pp; English.
XX
CC The invention relates to isolated polynucleotide (I) and polypeptide (II)
CC sequences. (I) is useful as hybridisation probes, polymerase chain
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
CC and in recombinant production of (II). The polynucleotides are also used
CC in diagnostics as expressed sequence tags for identifying expressed
CC genes. (I) is useful in gene therapy techniques to restore normal
CC activity of (II) or to treat disease states involving (II). (II) is
CC useful for generating antibodies against it, detecting or quantitating a
CC polypeptide in tissue, as molecular weight markers and as a food
CC supplement. (II) and its binding partners are useful in medical imaging
CC of sites expressing (II). (I) and (II) are useful for treating disorders
CC involving aberrant protein expression or biological activity. The
CC polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic
CC coding sequences of the invention. Note: The sequence data for this
CC patent did not appear in the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp://wipo.int/pub/published_pct_sequences
XX
SQ Sequence 1337 BP; 390 A; 305 C; 318 G; 324 T; 0 U; 0 Other;

Query Match 71.6%; Score 780; DB 5; Length 1337;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 780; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 311 CCACCTCCAGATCGAGAAGCTCTTGAACAAACCTGGACTGAAATATAAACCAAGTGACTAA 370
|||
Db 558 CCACCTCCAGATCGAGAAGCTCTTGAACAAACCTGGACTGAAATATAAACCAAGTGACTAA 617
|||
Qy 371 CCAGGTTGAGTGTACCCATACCTCACGCAGGAGAACTGATCCAGTACTGCCACTCCAA 430
|||
Db 618 CCAGGTTGAGTGTACCCATACCTCACGCAGGAGAACTGATCCAGTACTGCCACTCCAA 677
|||
Qy 431 GGGCATACCGTTACGGCCTACAGCCCCCTGGCTCTCCGGATAGACCTGGCCAAGCC 490
|||
Db 678 GGGCATACCGTTACGGCCTACAGCCCCCTGGCTCTCCGGATAGACCTGGCCAAGCC 737
|||
Qy 491 AGAAGACCCCTCCCTGCTGGAGGATCCCAAGATTAAGGAGATTGCTGCAAAGCACAAAAA 550
|||
Db 738 AGAAGACCCCTCCCTGCTGGAGGATCCCAAGATTAAGGAGATTGCTGCAAAGCACAAAAA 797
|||
Qy 551 AACCGCAGCCCAGGTTCTGATCCGTTCCATATCCAGAGGAATGTGATTGTCATCCCCAA 610
|||
Db 798 AACCGCAGCCCAGGTTCTGATCCGTTCCATATCCAGAGGAATGTGATTGTCATCCCCAA 857
|||

us-10-653-681b-1.oligo.rng

Qy	611	GTCTGTGACACCAGCACGCATTGTTGAGAACATTCAAGGTCTTGACTTTAAATTGAGTGA	670
Db	858	GTCTGTGACACCAGCACGCATTGTTGAGAACATTCAAGGTCTTGACTTTAAATTGAGTGA	917
Qy	671	TGAGGAGATGGCAACCATACTCAGCTTCAACAGAAAAGTGGAGGGCTGTAACGTGTTGCA	730
Db	918	TGAGGAGATGGCAACCATACTCAGCTTCAACAGAAAAGTGGAGGGCTGTAACGTGTTGCA	977
Qy	731	ATCCTCTCATTTGGAAGACTATCCCTCGATGCGAGAATATTGAGGTTGAATCTCTGGTG	790
Db	978	ATCCTCTCATTTGGAAGACTATCCCTCGATGCGAGAATATTGAGGTTGAATCTCTGGTG	1037
Qy	791	AGATTATAACAGGAGATTCTCTTCTCGCTGAAGTGTGACTACCTCCACTCATGTCCCAT	850
Db	1038	AGATTATAACAGGAGATTCTCTTCTCGCTGAAGTGTGACTACCTCCACTCATGTCCCAT	1097
Qy	851	TTTAGCCAAGCTTATTAAGATCACAGTGAACCTAGTCCTGTTAGACGAGAACATCGAGG	910
Db	1098	TTTAGCCAAGCTTATTAAGATCACAGTGAACCTAGTCCTGTTAGACGAGAACATCGAGG	1157
Qy	911	TGCTGTTTAGACATTTATTCTGTATGTTCAACTAGGATCAGAATATCACAGAAAAGCA	970
Db	1158	TGCTGTTTAGACATTTATTCTGTATGTTCAACTAGGATCAGAATATCACAGAAAAGCA	1217
Qy	971	TGGCTTGAATAAGGAAATGACAATTTCACCTTATCTGATCAGAACAAATGTTATTA	1030
Db	1218	TGGCTTGAATAAGGAAATGACAATTTCACCTTATCTGATCAGAACAAATGTTATTA	1277
Qy	1031	AGCATCAGAAACTCTGCCAACACTGAGGATGAAAGATCAATAAAAAAAATAATCAT	1090
Db	1278	AGCATCAGAAACTCTGCCAACACTGAGGATGAAAGATCAATAAAAAAAATAATCAT	1337

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OM nucleic - nucleic search, using sw model

Run on: August 9, 2005, 11:53:34 ; Search time 4250 Seconds
(without alignments)
9762.366 Million cell updates/sec

Title: US-10-653-681B-1

Perfect score: 1090

Sequence: 1 caaaaacacgcaacagaaaagc.....ataaaaaaaaataataatcat 1090

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 34239544 seqs, 19032134700 residues

Word size : 0

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : EST:*

- 1: gb_est1:*
- 2: gb_est2:*
- 3: gb_htc:*
- 4: gb_est3:*
- 5: gb_est4:*
- 6: gb_est5:*
- 7: gb_est6:*
- 8: gb_gss1:*
- 9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

8

Result	Query					Description	
No.	Score	Match	Length	DB	ID		
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c 1	629	57.7	735	5	BM981698	BM981698 UI-CF-EN1	
	2	585	53.7	613	6	CB132708	CB132708 K-EST0183
c 3	570	52.3	593	5	BU677104	BU677104 UI-CF-DU1	
	4	517	47.4	588	2	BE785963	BE785963 601478213
c 5	496	45.5	540	1	AA804597	AA804597 nk97e06.s	
	6	493	45.2	623	4	BM793014	BM793014 K-EST0073
c 7	479	43.9	595	5	BM983180	BM983180 UI-CF-EN1	
c 8	454	41.7	644	6	CA450136	CA450136 UI-CF-FN0	

c 9	446	40.9	456	1	AI292337	AI292337 qm77c02.x
c 10	446	40.9	458	1	AI744504	AI744504 wg09a09.x
c 11	446	40.9	460	1	AI291463	AI291463 qm73h04.x
c 12	444	40.7	452	1	AI393702	AI393702 tg66d01.x
c 13	432	39.6	446	5	BX104876	BX104876 BX104876
14	431	39.5	592	4	BM819663	BM819663 K-EST0087
c 15	426	39.1	448	5	BM975664	BM975664 UI-CF-EN1
16	417	38.3	445	6	CB161124	CB161124 K-EST0220
17	401	36.8	635	7	CV334625	CV334625 IL3-UT011
18	400	36.7	620	6	CB118695	CB118695 K-EST0165
c 19	392	36.0	746	2	BF688991	BF688991 602185236
20	385	35.3	453	4	BG197874	BG197874 RST17122
c 21	378	34.7	388	1	AI831519	AI831519 wj49h11.x
c 22	363	33.3	445	1	AI301329	AI301329 qn27e09.x
c 23	363	33.3	496	2	AW379341	AW379341 MR0-HT024
24	361	33.1	384	2	BE787870	BE787870 601479812
25	360	33.0	796	4	BG682196	BG682196 602629503
c 26	345	31.7	388	2	BE711936	BE711936 QV2-HT069
27	341	31.3	485	7	CV334678	CV334678 IL3-UT011
c 28	338	31.0	415	1	AA947514	AA947514 oq53h01.s
29	329	30.2	786	5	BQ221381	BQ221381 AGENCOURT
30	324	29.7	365	5	BQ377471	BQ377471 IL2-UM007
31	319	29.3	319	4	BM855292	BM855292 K-EST0138
32	316	29.0	729	5	BX480365	BX480365 DKF2p6860
33	316	29.0	1177	4	BM558121	BM558121 AGENCOURT
c 34	314	28.8	666	1	AI924753	AI924753 wn58a02.x
c 35	300	27.5	300	1	AI270664	AI270664 qu90c04.x
c 36	299	27.4	549	5	BQ315282	BQ315282 RC3-IT001
37	299	27.4	909	4	BG169378	BG169378 602320937
38	296	27.2	316	5	BU175462	BU175462 AGENCOURT
39	295	27.1	310	4	BM783186	BM783186 K-EST0061
c 40	292	26.8	346	2	BE775022	BE775022 IL2-UM007
41	285	26.1	582	5	BP278752	BP278752 BP278752
42	280	25.7	581	5	BP263763	BP263763 BP263763
43	272	25.0	912	5	BQ220848	BQ220848 AGENCOURT
44	248	22.8	535	6	CB147729	CB147729 K-EST0203
45	248	22.8	557	4	BG490449	BG490449 602519494

ALIGNMENTS

RESULT 1

BM981698/c

LOCUS BM981698 735 bp mRNA linear EST 21-FEB-2003
 DEFINITION UI-CF-EN1-adi-f-17-0-UI.s1 UI-CF-EN1 Homo sapiens cDNA clone
 UI-CF-EN1-adi-f-17-0-UI 3', mRNA sequence.
 ACCESSION BM981698
 VERSION BM981698.1 GI:19604453
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 735)
 AUTHORS Bonaldo, M.F., Lennon, G. and Soares, M.B.
 TITLE Normalization and subtraction: two approaches to facilitate gene

discovery
JOURNAL Genome Res. 6 (9), 791-806 (1996)
MEDLINE 97044477
PUBMED 8889548
COMMENT Contact: McCray, PB
McCray Lab
University of Iowa
2024 University of Iowa Med Labs, Iowa City, IA 52242, USA
Tel: 319 356 4866
Fax: 319 356 7171
Email: paul-mccray@uiowa.edu
Tissue Procurement: Dr. M. J. Welsh, University of Iowa
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com) or from Open Biosystems
(www.openbiosystems.com).
The following repetitive elements were found in this cDNA
sequence: 1-44, >POLY_A#Simple_repeat (matched compliment)
Seq primer: M13 FORWARD
POLYA=Yes.

FEATURES Location/Qualifiers
source 1. .735
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-CF-EN1-adi-f-17-0-UI"
/tissue_type="Primary Lung Cystic Fibrosis Epithelial
Cells"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies) (T1 phage resistant)"
/clone_lib="UI-CF-EN1"
/note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a
modified polylinker; Site_1: EcoR I; Site_2: Not I;
UI-CF-EN1 is a normalized cDNA library containing the
following tissue(s): Primary Lung Cystic Fibrosis
Epithelial Cells. The library was constructed according to
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. First strand cDNA synthesis was primed with an
oligo-dT primer containing a Not I site. Double stranded
cDNA was ligated to an EcoR I adaptor, digested with Not
I, and cloned directionally into pT7T3-Pac vector. The
oligonucleotide used to prime the synthesis of
first-strand cDNA contains a library tag sequence that is
located between the Not I site and the (dT)18 tail. The
sequence tag for this library is CTGCTCAGGT.
TAG_TISSUE=Human Lung Epithelial Cell Lines untreated LPS
6hr to LPS 24h
TAG_LIB=UI-CF-EN1
TAG_SEQ=CTGCTCAGGT"

ORIGIN

Query Match 57.7%; Score 629; DB 5; Length 735;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 629; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 462 GGCTCTCCGGATAGACCTGGGCCAAGCCAGAAGACCCTCCCTGCTGGAGGATCCAAG 521
|||
Db 645 GGCTCTCCGGATAGACCTGGGCCAAGCCAGAAGACCCTCCCTGCTGGAGGATCCAAG 586
|||
Qy 522 ATTAAGGAGATTGCTGCAAAGCACAAAAACCGCAGCCAGGTTCTGATCCGTTCCAT 581
|||
Db 585 ATTAAGGAGATTGCTGCAAAGCACAAAAACCGCAGCCAGGTTCTGATCCGTTCCAT 526
|||
Qy 582 ATCCAGAGGAATGTGATTGTCATCCCCAAGTCTGTGACACCAGCACGCATTGTTGAGAAC 641
|||
Db 525 ATCCAGAGGAATGTGATTGTCATCCCCAAGTCTGTGACACCAGCACGCATTGTTGAGAAC 466
|||
Qy 642 ATTCAAGGTCTTGACTTAAATTGAGTGATGAGGAGATGGCAACCATACTCAGCTTCAAC 701
|||
Db 465 ATTCAAGGTCTTGACTTAAATTGAGTGATGAGGAGATGGCAACCATACTCAGCTTCAAC 406
|||
Qy 702 AGAAACTGGAGGGCCTGTAACGTGTTGCAATCCTCTCATTGGAAGACTATCCCTCGAT 761
|||
Db 405 AGAAACTGGAGGGCCTGTAACGTGTTGCAATCCTCTCATTGGAAGACTATCCCTCGAT 346
|||
Qy 762 GCAGAATATTGAGGTTGAATCTCCTGGTGAGATTATACAGGAGATTCTCTTCGCTG 821
|||
Db 345 GCAGAATATTGAGGTTGAATCTCCTGGTGAGATTATACAGGAGATTCTCTTCGCTG 286
|||
Qy 822 AAGTGTGACTACCTCCACTCATGTCCCATTAGCCAAGCTTATTAAAGATCACAGTGAA 881
|||
Db 285 AAGTGTGACTACCTCCACTCATGTCCCATTAGCCAAGCTTATTAAAGATCACAGTGAA 226
|||
Qy 882 CTTAGTCCTGTTATAGACGAGAATCGAGGTGCTGTTTAGACATTATTCGTATGTT 941
|||
Db 225 CTTAGTCCTGTTATAGACGAGAATCGAGGTGCTGTTTAGACATTATTCGTATGTT 166
|||
Qy 942 AACTAGGATCAGAATATCACAGAAAAGCATGGCTTGAATAAGGAAATGACAATTTC 1001
|||
Db 165 AACTAGGATCAGAATATCACAGAAAAGCATGGCTTGAATAAGGAAATGACAATTTC 106
|||
Qy 1002 ACTTATCTGATCAGAACAAATGTTATTAAAGCATCAGAAACTCTGCCAACACTGAGGATG 1061
|||
Db 105 ACTTATCTGATCAGAACAAATGTTATTAAAGCATCAGAAACTCTGCCAACACTGAGGATG 46
|||
Qy 1062 TAAAGATCAATAAAAAAAATAATAATCAT 1090
|||
Db 45 TAAAGATCAATAAAAAAAATAATAATCAT 17

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OM nucleic - nucleic search, using sw model

Run on: August 9, 2005, 06:02:48 ; Search time 5146 Seconds
(without alignments)
10263.542 Million cell updates/sec

Title: US-10-653-681B-1
Perfect score: 1090
Sequence: 1 caaaaacagcaacagaaagc.....ataaaaaaaaataataatcat 1090

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*

1: gb_ba:*

2: gb_htg:*

3: gb_in:*

4: gb_om:*

5: gb_ov:*

6: gb_pat:*

7: gb_ph:*

8: gb_pl:*

9: gb_pr:*

10: gb_ro:*

11: gb_sts:*

12: gb_sy:*

13: gb_un:*

14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%

Result	Query					Description
No.	Score	Match	Length	DB	ID	
1	833	76.4	1337	9	HSU37100	U37100 Homo sapien
2	830.8	76.2	1336	6	CQ718316	CQ718316 Sequence

3	828.2	76.0	1551	9	BC008837	BC008837	Homo sapi
4	828.2	76.0	1560	6	CQ776685	CQ776685	Sequence
5	820.2	75.2	1611	9	AF524864	AF524864	Homo sapi
6	796.6	73.1	1316	6	AR272611	AR272611	Sequence
7	796.6	73.1	1316	6	AR276192	AR276192	Sequence
8	796.6	73.1	1316	6	AR406467	AR406467	Sequence
9	796.6	73.1	1316	6	AR440317	AR440317	Sequence
10	796.6	73.1	1316	6	AR472475	AR472475	Sequence
11	796.6	73.1	1316	6	AR543128	AR543128	Sequence
12	796.6	73.1	1316	6	AX062696	AX062696	Sequence
13	796.6	73.1	1316	6	AX367613	AX367613	Sequence
14	796.6	73.1	1316	9	AF052577	AF052577	Homo sapi
15	718.	65.9	1315	6	AX743782	AX743782	Sequence
16	651.8	59.8	3994	9	AL669847	AL669847	Human DNA
17	651.8	59.8	121210	9	AL607022	AL607022	Human DNA
18	574	52.7	574	9	AF044961	AF044961	Homo sapi
19	508	46.6	1080	6	AX772965	AX772965	Sequence
20	459.4	42.1	951	9	BT006794	BT006794	Homo sapi
21	459.4	42.1	951	12	BT007750	BT007750	Synthetic
22	458.4	42.1	948	9	CR541801	CR541801	Homo sapi
23	431	39.5	951	6	AX380448	AX380448	Sequence
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ALIGNMENTS

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LOCUS HSU37100 1337 bp mRNA linear PRI 28-MAY-1998
DEFINITION Homo sapiens aldose reductase-like peptide mRNA, complete cds.
ACCESSION U37100
VERSION U37100.1 GI:3150034
KEYWORDS

SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 1337)
 AUTHORS Cao, D., Fan, S.T. and Chung, S.S.
 TITLE Identification and characterization of a novel human aldose
 reductase-like gene
 JOURNAL J. Biol. Chem. 273 (19), 11429-11435 (1998)
 MEDLINE 98234319
 PUBMED 9565553
 REFERENCE 2 (bases 1 to 1337)
 AUTHORS Cao, D.
 TITLE Direct Submission
 JOURNAL Submitted (27-SEP-1995) Deliang Cao, The University of Hong Kong,
 Institute of Molecular Biology, 8 Sassoon Road, Pokfulam, Hong
 Kong, Hong Kong
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 /db_xref="GI:3150035"

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 NFSHQIEKLLNKPGKLYKPVTNQVECHPYLTQEKLIQYCHSKGITVTAYSPLGSPDR
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 Best Local Similarity 81.5%; Pred. No. 1.4e-221;
 Matches 1090; Conservative 0; Mismatches 0; Indels 247; Gaps 1;

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Qy 1074 AAAAAAATAATAATCAT 1090
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Db 1321 AAAAAAATAATAATCAT 1337

us-10-653-681b-1.rng

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OM nucleic - nucleic search, using sw model

Run on: August 9, 2005, 05:31:49 ; Search time 697 seconds
(without alignments)
9257.558 Million cell updates/sec

Title: US-10-653-681B-1

Perfect score: 1090

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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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8: geneseqn2003as:
9: geneseqn2003bs:
10: geneseqn2003cs:
11: geneseqn2003ds:
12: geneseqn2004as:
13: geneseqn2004bs:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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5	828.2	76.0	1560	12	ADN04246	Adn04246 Antipsori
6	828.2	76.0	1560	13	ACN38728	Acn38728 Tumour-as
7	828.2	76.0	1560	13	ADS85007	Ads85007 Human ato
8	822.8	75.5	1549	12	ADK70274	Adk70274 Respirato
9	796.6	73.1	1316	5	AAF68405	Aaf68405 Human lun
10	796.6	73.1	1316	6	ABK38316	Abk38316 cDNA enco

us-10-653-681b-1.rng									
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12	796.6	73.1	1316	8	ACA10645				Aca10645 Human lun
13	796.6	73.1	1316	8	ABX99596				Abx99596 Lung canc
14	796.6	73.1	1316	10	ADH45842				Adh45842 Human lun
15	796.6	73.1	1316	12	ADE72379				Ade72379 Human lun
16	796.6	73.1	1316	13	ADJ19761				Adj19761 Human lun
17	770.8	70.7	1621	12	ADH13722				Adh13722 Human ENZ
18	718	65.9	1315	10	ADC97771				Adc97771 Human ARL
19	635.4	58.3	1816	11	ACN92921				Acn92921 Breast ca
20	616	56.5	770	13	ADR98739				Adr98739 Lung spec
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ALIGNMENTS

RESULT 1

AAS68608

ID AAS68608 standard; cDNA; 1337 BP.

xx

AC AAS68608;

xx

DT 13-FEB-2002 (first entry)

xx

RNA encoding novel human diagnostic protein #4412

DE
XX

KW Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss.

xx

OS *Homo sapiens.*

xx

PN WO200175067-A2.

xx

11.08.2001

PDB
100

RE 30-MAR-2001: 2001WO-US008631

PF
XX

PR 31-MAR-2000: 2000US-00540217.

PR

TR 25 AUG 2000, 200003 00049107.

XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Drmanac RT, Liu C, Tang YT;
 XX
 DR WPI; 2001-639362/73.
 DR P-PSDB; ABG04421.
 XX
 PT New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity.
 XX
 PS Claim 1; SEQ ID NO 4412; 103pp; English.
 XX
 CC The invention relates to isolated polynucleotide (I) and polypeptide (II)
 CC sequences. (I) is useful as hybridisation probes, polymerase chain
 CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
 CC and in recombinant production of (II). The polynucleotides are also used
 CC in diagnostics as expressed sequence tags for identifying expressed
 CC genes. (I) is useful in gene therapy techniques to restore normal
 CC activity of (II) or to treat disease states involving (II). (II) is
 CC useful for generating antibodies against it, detecting or quantitating a
 CC polypeptide in tissue, as molecular weight markers and as a food
 CC supplement. (II) and its binding partners are useful in medical imaging
 CC of sites expressing (II). (I) and (II) are useful for treating disorders
 CC involving aberrant protein expression or biological activity. The
 CC polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic
 CC coding sequences of the invention. Note: The sequence data for this
 CC patent did not appear in the printed specification, but was obtained in
 CC electronic format directly from WIPO at
 CC ftp://wipo.int/pub/published_pct_sequences
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 Query Match 76.4%; Score 833; DB 5; Length 1337;
 Best Local Similarity 81.5%; Pred. No. 1.1e-230;
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Db	841 GTGATTGTCATCCCCAAGTCTGTGACACCCAGCAGCATTGTTGAGAACATTAGGTCTTT	900
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us-10-653-681b-1.rng

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Qy 1074 AAAAAAATAATAATCAT 1090
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Db 1321 AAAAAAATAATAATCAT 1337

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 9, 2005, 07:25:59 ; Search time 4248 Seconds
(without alignments)
9766.962 Million cell updates/sec

Title: US-10-653-681B-1

Perfect score: 1090

Sequence: 1 caaaaacacgcaacagaaaagc.....ataaaaaaaaataataatcat 1090

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: gb_est2:*

3: gb_htc:*

4: gb_est3:*

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6: gb_est5:*

7: gb_est6:*

8: gb_gss1:*

9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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c	3	666	61.1	746	2	BF688991		BF688991 602185236
c	4	652.2	59.8	796	5	BX337598		BX337598 BX337598
	5	647	59.4	909	4	BG169378		BG169378 602320937
c	6	586.6	53.8	666	1	AI924753		AI924753 wn58a02.x
	7	585	53.7	613	6	CB132708		CB132708 K-EST0183
c	8	573	52.6	595	5	BM983180		BM983180 UI-CF-EN1

c	9	570.8	52.4	593	5	BU677104	BU677104	UI-CF-DU1
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	17	502.6	46.1	704	7	CO582646	CO582646	ILLUMIGEN
	18	498.8	45.8	620	6	CB118695	CB118695	K-EST0165
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	28	446.4	41.0	582	5	BP278752	BP278752	BP278752
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c	30	426.6	39.1	445	1	AI301329	AI301329	qn27e09.x
	31	426.4	39.1	914	7	CO775128	CO775128	ILLUMIGEN
c	32	426	39.1	448	5	BM975664	BM975664	UI-CF-EN1
	33	417	38.3	445	6	CB161124	CB161124	K-EST0220
	34	402.4	36.9	581	5	BP263763	BP263763	BP263763
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	36	388.8	35.7	453	4	BG197874	BG197874	RST17122
	37	384.8	35.3	912	5	BQ220848	BQ220848	AGENCOURT
c	38	383.4	35.2	405	6	C75075	C75075	C75075 Huma
c	39	378	34.7	388	1	AI831519	AI831519	wj49h11.x
	40	373	34.2	384	2	BE787870	BE787870	601479812
c	41	370.6	34.0	386	1	AI813308	AI813308	wj33c01.x
c	42	365.2	33.5	388	2	BE711936	BE711936	QV2-HT069
	43	360	33.0	796	4	BG682196	BG682196	602629503
	44	351.2	32.2	1342	3	AK075865	AK075865	Mus muscu
	45	348	31.9	1236	3	AK019906	AK019906	Mus muscu

us-10-653-681b-1.oligo.rni

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OM nucleic - nucleic search, using sw model

Run on: August 9, 2005, 08:31:19 ; Search time 227 Seconds
(without alignments)
7857.012 Million cell updates/sec

Title: US-10-653-681B-1

Perfect score: 1090

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Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 1202784 seqs, 818138359 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	664	60.9	1316	4	US-09-702-705-323	Sequence 323, App
3	664	60.9	1316	4	US-09-736-457-323	Sequence 323, App
4	664	60.9	1316	4	US-09-614-124B-323	Sequence 323, App
5	664	60.9	1316	4	US-09-671-325-323	Sequence 323, App
6	664	60.9	1316	4	US-09-589-184-323	Sequence 323, App
7	664	60.9	1316	4	US-09-658-824-323	Sequence 323, App
8	331	30.4	17740	4	US-09-949-016-13086	Sequence 13086, A
9	316	29.0	585	3	US-09-123-912-92	Sequence 92, Appl
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15	316	29.0	585	4	US-09-466-396A-92	Sequence 92, Appl
16	316	29.0	585	4	US-09-476-496A-92	Sequence 92, Appl
17	316	29.0	585	4	US-09-630-940B-92	Sequence 92, Appl

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c 18	316	29.0	585	4	US-09-285-479-92	Sequence 92, Appl
c 19	316	29.0	858	3	US-09-123-912-91	Sequence 91, Appl
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ALIGNMENTS

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; Sequence 1344, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1344
; LENGTH: 1515
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-1344

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Best Local Similarity 99.9%; Pred. No. 0;
Matches 779; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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5	664	60.9	1316	9	US-09-902-941-323	Sequence 323, App
6	664	60.9	1316	9	US-09-849-626-323	Sequence 323, App
7	664	60.9	1316	10	US-09-476-300-323	Sequence 323, App
8	664	60.9	1316	14	US-10-017-754-323	Sequence 323, App
9	664	60.9	1316	15	US-10-102-524-1731	Sequence 1731, Ap
10	664	60.9	1316	16	US-10-113-872-323	Sequence 323, App
11	664	60.9	1316	17	US-10-283-017-323	Sequence 323, App
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37	159	14.6	1315	15	US-10-274-375-1	Sequence 1, Appl
38	144	13.2	233	9	US-09-736-457-31	Sequence 31, Appl
39	144	13.2	233	9	US-09-902-941-31	Sequence 31, Appl
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41	144	13.2	233	10	US-09-476-300-31	Sequence 31, Appl
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43	144	13.2	233	16	US-10-113-872-31	Sequence 31, Appl
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ALIGNMENTS

RESULT 1

US-10-653-681A-1

; Sequence 1, Application US/10653681A

; Publication No. US20050048503A1

; GENERAL INFORMATION:

; APPLICANT: DAI, KEN-SHWO

; TITLE OF INVENTION: HUMAN ARL-RELATED GENE VARIANTS ASSOCIATED WITH CANCER

; FILE REFERENCE: U014798-3

; CURRENT APPLICATION NUMBER: US/10/653,681A

; CURRENT FILING DATE: 2003-09-02

us-10-653-681b-1.oligo.rnpb

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LENGTH: 1090
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ORGANISM: ARTIFICIAL SEQUENCE
FEATURE:
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US-10-653-681A-1

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Matches 1090; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	828.2	76.0	1515	4	US-09-949-016-1344	Sequence 1344, Ap
2	796.6	73.1	1316	4	US-09-702-705-323	Sequence 323, App
3	796.6	73.1	1316	4	US-09-736-457-323	Sequence 323, App
4	796.6	73.1	1316	4	US-09-614-124B-323	Sequence 323, App
5	796.6	73.1	1316	4	US-09-671-325-323	Sequence 323, App
6	796.6	73.1	1316	4	US-09-589-184-323	Sequence 323, App
7	796.6	73.1	1316	4	US-09-658-824-323	Sequence 323, App
8	389.2	35.7	914	4	US-09-949-016-3127	Sequence 3127, Ap
9	358.4	32.9	17740	4	US-09-949-016-13086	Sequence 13086, A
10	328.6	30.1	601	4	US-09-949-016-46452	Sequence 46452, A
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12	316	29.0	585	3	US-09-643-597-92	Sequence 92, Appl
13	316	29.0	585	4	US-09-480-884A-92	Sequence 92, Appl
14	316	29.0	585	4	US-09-542-615A-92	Sequence 92, Appl
15	316	29.0	585	4	US-09-606-421B-92	Sequence 92, Appl
16	316	29.0	585	4	US-09-221-107-92	Sequence 92, Appl
17	316	29.0	585	4	US-09-466-396A-92	Sequence 92, Appl

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18	316	29.0	585	4	US-09-476-496A-92	Sequence 92, Appl
19	316	29.0	585	4	US-09-630-940B-92	Sequence 92, Appl
20	316	29.0	585	4	US-09-285-479-92	Sequence 92, Appl
c 21	316	29.0	858	3	US-09-123-912-91	Sequence 91, Appl
c 22	316	29.0	858	3	US-09-643-597-91	Sequence 91, Appl
c 23	316	29.0	858	4	US-09-480-884A-91	Sequence 91, Appl
c 24	316	29.0	858	4	US-09-542-615A-91	Sequence 91, Appl
c 25	316	29.0	858	4	US-09-606-421B-91	Sequence 91, Appl
c 26	316	29.0	858	4	US-09-221-107-91	Sequence 91, Appl
c 27	316	29.0	858	4	US-09-466-396A-91	Sequence 91, Appl
c 28	316	29.0	858	4	US-09-476-496A-91	Sequence 91, Appl
c 29	316	29.0	858	4	US-09-630-940B-91	Sequence 91, Appl
c 30	316	29.0	858	4	US-09-285-479-91	Sequence 91, Appl
31	304.8	28.0	1335	4	US-09-023-655-1010	Sequence 1010, Ap
32	292	26.8	1337	3	US-08-801-344-3	Sequence 3, Appl
33	292	26.8	1337	3	US-09-498-599-3	Sequence 3, Appl
34	288.4	26.5	601	4	US-09-949-016-46451	Sequence 46451, A
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37	165.4	15.2	601	4	US-09-949-016-46442	Sequence 46442, A
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39	145.4	13.3	233	4	US-09-702-705-31	Sequence 31, Appl
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41	145.4	13.3	233	4	US-09-614-124B-31	Sequence 31, Appl
42	145.4	13.3	233	4	US-09-671-325-31	Sequence 31, Appl
43	145.4	13.3	233	4	US-09-589-184-31	Sequence 31, Appl
44	145.4	13.3	233	4	US-09-658-824-31	Sequence 31, Appl
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ALIGNMENTS

RESULT 1

US-09-949-016-1344

; Sequence 1344, Application US/09949016

; Patent No. 6812339

; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

; FILE REFERENCE: CL001307

; CURRENT APPLICATION NUMBER: US/09/949,016

; CURRENT FILING DATE: 2000-04-14

; PRIOR APPLICATION NUMBER: 60/241,755

; PRIOR FILING DATE: 2000-10-20

; PRIOR APPLICATION NUMBER: 60/237,768

; PRIOR FILING DATE: 2000-10-03

; PRIOR APPLICATION NUMBER: 60/231,498

; PRIOR FILING DATE: 2000-09-08

; NUMBER OF SEQ ID NOS: 207012

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 1344

; LENGTH: 1515

; TYPE: DNA

; ORGANISM: Human

US-09-949-016-1344

Query Match 76.0%; Score 828.2; DB 4; Length 1515;
 Best Local Similarity 81.3%; Pred. No. 1.2e-247;
 Matches 1087; Conservative 0; Mismatches 3; Indels 247; Gaps 1;

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Qy	121	CTGGGACTTGGAAAGTCTCCTCTCGGCAAAGTGAAGAAGCAGTGAAGGTGGCATTGAT	180
Db	299	CTGGGACTTGGAAAGTCTCCTCTGGCAAAGTGAAGAAGCAGTGAAGGTGGCATTGAT	358
Qy	181	GCAGGATATCGGCACATTGACTGTGCCTATGTCTATCAGAACATGAAGTGGGGAA	240
Db	359	GCAGGATATCGGCACATTGACTGTGCCTATGTCTATCAGAACATGAAGTGGGGAA	418
Qy	241	GCCATCCAAGAGAAGATCCAAGAGAAGGCTGTGAAGCGGGAGGACCTGTTCATCGTCAGC	300
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Qy	301	AAGTTGTGGC-----	310
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Db	599	TCTGGGATGACCTTTCCCCAAAGATGATAAAGGTAATGCCATCGTGGAAAAGCAACG	658
Qy	311	-----	310
Db	659	TTCTTGATGCCTGGAGGCCATGGAGGAGCTGGTGATGAGGGCTGGTGAAGCCCTT	718
Qy	311	-----CCACTTCCAGATCGAGAAGCTCTGAACAAACCTGGACTGAAA	353
Db	719	GGGGTCTCCAATTCAGCCACTTCCAGATCGAGAAGCTCTGAACAAACCTGGACTGAAA	778
Qy	354	TATAAACCAAGTACTAACCAAGGTTGAGTGTACCCATACCTCACGCAGGAGAAACTGATC	413
Db	779	TATAAACCAAGTACTAACCAAGGTTGAGTGTACCCATACCTCACGCAGGAGAAACTGATC	838
Qy	414	CAGTAUTGCCACTCCAAGGCATACCGTTACGGCTACAGCCCCCTGGGCTCTCCGGAT	473
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Qy	474	AGACCTTGGCCAAGCCAGAAGACCCCTCCCTGCTGGAGGATCCAAAGATTAAAGGAGATT	533
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Qy	534	GCTGCAAAGCACAAAAAACCGCAGCCAGGTTCTGATCCGTTCCATATCCAGAGGAAT	593
Db	959	GCTGCAAAGCACAAAAAACCGCAGCCAGGTTCTGATCCGTTCCATATCCAGAGGAAT	1018
Qy	594	GTGATTGTATCCCCAAGTCTGTGACACCAAGCAGCATTGTTGAGAACATTCAAGGTCTT	653
Db	1019	GTGATTGTATCCCCAAGTCTGTGACACCAAGCAGCATTGTTGAGAACATTCAAGGTCTT	1078
Qy	654	GACTTTAAATTGAGTGTGAGGAGATGGCAACCATACTCAGCTCAACAGAAACTGGAGG	713
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Qy	714	GCCTGTAACGTGTTGCAATCCTCTCATTTGGAAGACTATCCCTTCGATGCAGAATATTGA	773
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Qy	774	GGTTGAATCTCCTGGTGGAGATTATACAGGGAGATTCTCTTCGCTGAAGTGTGACTAC	833
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Qy	894	ATAGACGAGAATCGAGGTGCTGTTTAGACATTTAGACATTTCTGTATGTTCAACTAGGATCAG	953
Db	1319	ATAGACGAGAATCGAGGTGCTGTTTAGACATTTAGACATTTCTGTATGTTCAACTAGGATCAG	1378
Qy	954	AATATCACAGAAAAGCATGGCTTGAATAAGGAAATGACAATTTTCCACTTATCTGATC	1013
Db	1379	AATATCACAGAAAAGCATGGCTTGAATAAGGAAATGACAATTTTCCACTTATCTGATC	1438
Qy	1014	AGAACAAATGTTATTAAGCATCAGAAACTCTGCCAACACTGAGGATGAAAGATCAATA	1073
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Qy	1074	AAAAAAAATAATAATCAT	1090
Db	1499	AAAAAAAATAATAATCAT	1515

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OM nucleic - nucleic search, using sw model

Run on: August 9, 2005, 06:00:04 ; Search time 1792 Seconds
(without alignments)
3942.932 Million cell updates/sec

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Perfect score: 1090

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Gapop 10.0 , Gapext 1.0

Searched: 7297361 seqs, 3241162794 residues

Total number of hits satisfying chosen parameters: 14594722

Minimum DB seq length: 0

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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us-10-653-681b-1.rnpb

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4	796.6	73.1	1316	9	US-09-736-457-323	Sequence 323, App
5	796.6	73.1	1316	9	US-09-902-941-323	Sequence 323, App
6	796.6	73.1	1316	9	US-09-849-626-323	Sequence 323, App
7	796.6	73.1	1316	10	US-09-476-300-323	Sequence 323, App
8	796.6	73.1	1316	14	US-10-017-754-323	Sequence 323, App
9	796.6	73.1	1316	15	US-10-102-524-1731	Sequence 1731, Ap
10	796.6	73.1	1316	16	US-10-113-872-323	Sequence 323, App
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12	718	65.9	1315	15	US-10-274-375-1	Sequence 1, Appl
13	707	64.9	1279	21	US-10-653-681A-3	Sequence 3, Appl
14	635.4	58.3	1816	14	US-10-198-846-14071	Sequence 14071, A
15	431	39.5	951	15	US-10-274-694-36	Sequence 36, Appl
16	431	39.5	951	20	US-10-332-448-36	Sequence 36, Appl
17	360.4	33.1	364	10	US-09-803-719-2393	Sequence 2393, Ap
18	353.4	32.4	356	10	US-09-803-719-2391	Sequence 2391, Ap
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21	316	29.0	585	9	US-09-897-778-92	Sequence 92, Appl
22	316	29.0	585	10	US-09-466-396A-92	Sequence 92, Appl
23	316	29.0	585	14	US-10-007-700-92	Sequence 92, Appl
24	316	29.0	585	15	US-10-117-982-92	Sequence 92, Appl
25	316	29.0	585	17	US-10-313-986-92	Sequence 92, Appl
26	316	29.0	585	20	US-10-775-972-92	Sequence 92, Appl
27	316	29.0	585	22	US-10-922-124-92	Sequence 92, Appl
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c 29	316	29.0	858	9	US-09-850-716A-91	Sequence 91, Appl
c 30	316	29.0	858	9	US-09-897-778-91	Sequence 91, Appl
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c 34	316	29.0	858	17	US-10-313-986-91	Sequence 91, Appl
c 35	316	29.0	858	20	US-10-775-972-91	Sequence 91, Appl
c 36	316	29.0	858	22	US-10-922-124-91	Sequence 91, Appl
37	304.8	28.0	1331	20	US-10-737-450-97	Sequence 97, Appl
38	304.8	28.0	1335	18	US-10-641-643-1010	Sequence 1010, Ap
39	304.8	28.0	1367	9	US-09-864-864-332	Sequence 332, App
40	304.8	28.0	1367	15	US-10-171-581-1	Sequence 1, Appl
41	304.8	28.0	1367	17	US-10-172-118-641	Sequence 641, App
42	304.8	28.0	1367	18	US-10-342-887-641	Sequence 641, App
43	304.8	28.0	1367	19	US-10-717-597-289	Sequence 289, App
44	304.8	28.0	1368	19	US-10-416-330-21	Sequence 21, Appl
45	304.8	28.0	1416	21	US-10-887-553A-128	Sequence 128, App

ALIGNMENTS

RESULT 1

US-10-653-681A-1

; Sequence 1, Application US/10653681A

; Publication No. US20050048503A1

GENERAL INFORMATION:

; APPLICANT: DAI, KEN-SHWO

; TITLE OF INVENTION: HUMAN ARL-RELATED GENE VARIANTS ASSOCIATED WITH CANCER

; FILE REFERENCE: U014798-3

; CURRENT APPLICATION NUMBER: US/10/653,681A

; CURRENT FILING DATE: 2003-09-02

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 SOFTWARE: PatentIn version 3.2
 SEQ ID NO 1
 LENGTH: 1090
 TYPE: DNA
 ORGANISM: ARTIFICIAL SEQUENCE
 FEATURE:
 OTHER INFORMATION: VARIANT OF HUMAN ALDOSE REDUCTASE-LIKE GENE
 FEATURE:
 NAME/KEY: CDS
 LOCATION: (70)..(333)
 US-10-653-681A-1

Query Match 100.0%; Score 1090; DB 21; Length 1090;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1090; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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